

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 12:54:48 ; Search time 209 Seconds
(without alignments)

2689.670 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977

Sequence: 1 MLLWILLVLAPVSGQFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	876	89.7	977	Q96RD9	Q96rd9 homo sapien
2	403	41.2	437	Q8NF56	Q8nf56 homo sapien
3	102	10.4	124	Q6UY46	Q6uy46 homo sapien
4	102	10.4	124	AAQ88452	AAQ88452 homo sapi
5	23	2.4	144	Q9BZ14	Q9bz14 homo sapien
6	23	2.4	192	Q9BZ15	Q9bz15 homo sapien
7	23	2.4	255	Q9BZ16	Q9bz16 homo sapien
8	23	2.4	508	Q96LA5	Q96la5 homo sapien
9	23	2.4	508	AAQ88497	AAQ88497 homo sapi
10	17	1.7	639	Q96P30	Q96p30 homo sapien
11	17	1.7	734	Q96LA4	Q96la4 homo sapien
12	17	1.7	734	Q96P31	Q96p31 homo sapien
13	17	1.7	740	Q96P29	Q96p29 homo sapien
14	17	1.7	742	Q8N6S2	Q8n6s2 homo sapien
15	15	1.5	366	Q8N759	Q8n759 homo sapien
16	15	1.5	428	Q96PJ6	Q96pj6 homo sapien
17	15	1.5	429	Q96LA6	Q96la6 homo sapien
18	14	1.4	154	Q8N733	Q8n733 homo sapien
19	14	1.4	508	Q8BJA5	Q8bja5 mus musculus
20	14	1.4	582	Q8OWN2	Q8own2 mus musculus
21	11	1.1	208	Q8OWN3	Q8own3 mus musculus
22	11	1.1	324	Q7TMH2	Q7tmh2 mus musculus
23	11	1.1	343	Q8BYS4	Q8bys4 mus musculus
24	11	1.1	343	Q8BAY0	Q8bay0 mus musculus
25	9	0.9	136	1XVSB_MOUSE	P01634 mus musculus
26	9	0.9	204	Q8CWD9	Q8cwd9 escherichia
27	9	0.9	215	Q82GY7	Q82gy7 streptomyces
28	9	0.9	311	Q6DN73	Q6dn73 homo sapien
29	9	0.9	397	Q6XRC3	Q6xrc3 homo sapien
30	9	0.9	397	2AAP47270	AAP47270 homo sapi
31	9	0.9	413	Q6ZNI1	Q6zni1 homo sapien

ALIGNMENTS

RESULT 1

ID	Q96RD9	PRELIMINARY;	PRT;	977 AA.
AC	Q96RD9;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Fc receptor-like protein 5.			
GN	Name=FCRH5;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21396562; PubMed=11493702;			
RA	Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;			
RT	"Identification of a family of Fc receptor homologs with preferential B cell expression.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).			
DR	EMBL; AF397453; AAI93971.1; -.			
DR	HSSP; F12319; IF2Q.			
DR	GO; GO:0004872; Fc receptor activity; IEA.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF00047; Ig; 8.			
DR	SMART; SM00408; Igc2; 1.			
DR	PROSITE; PS00835; IG_LIKE; 8.			
KW	Receptor.			
SQ	SEQUENCE 977 AA; 106496 MW; 24E4A027B25509E7 CRC64;			
Query Match 89.7%; Score 876; DB 2; Length 977;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 976; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	MLLWILLVLAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPOKTKWYHR	60	
Db	1	MLLWILLVLAPVSGQFARTPRPIIFLQPPWTVFQGERVLTCKGFRFYSPOKTKWYHR	60	
Qy	61	YLKGEILRETPDNI LVEQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEGDSVV	120	
Db	61	YLKGEILRETPDNI LVEQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEGDSVV	120	
Qy	121	LRCRAKAEVLTNNIYKNDNVLAFLNKRDTDFHIPHACLKNDGAYRGTGYNKSCCPVSSNT	180	
Db	121	LRCRAKAEVLTNNIYKNDNVLAFLNKRDTDFHIPHACLKNDGAYRGTGYNKSCCPVSSNT	180	
Qy	181	VKTQVQEPFTRPVLRASSFQPSGNPVLTTCETQLSLERSDVLPRFRFRDDOTLGLGWS	240	
Db	181	VKTQVQEPFTRPVLRASSFQPSGNPVLTTCETQLSLERSDVLPRFRFRDDOTLGLGWS	240	
Qy	241	LSPNFQITAMWSKDSGFYNCKAATMPHSVISDSFRSWIQVQIPASHPVLTLSPEKALNFE	300	
Db	241	LSPNFQITAMWSKDSGFYNCKAATMPHSVISDSFRSWIQVQIPASHPVLTLSPEKALNFE	300	

Badi8394 homo sapi
Q6dn72 homo sapien
Q9eqy5 m mman-g pr
Q91yk7 mus musculu
Q96kl5 homo sapien
Q96ny8 homo sapien
Aah10423 homo sapi
Q75ia9 ashbya goss
Aas54292 ashbya go
Q7uf18 rhodopirell
Q6bwb6 debaryomyce
Aar11051 mus muscu
Aar11058 mus muscu
Q9vz01 drosophila

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301 GTRKVTLLHCEQDLSRLTRFYHEGVPLRHKSVRCERGASISFSLTTTNSGNYICTADNG 360
301 GTRKVTLLHCEQDLSRLTRFYHEGVPLRHKSVRCERGASISFSLTTTNSGNYICTADNG 360
361 LGAKPSKAVSLSVTPVSHPVNLNLSPEGLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
361 LGAKPSKAVSLSVTPVSHPVNLNLSPEGLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
421 LRRSANSAGGVAISFSLTAHSGNYICTADNGFGPQRKAVSLITVPVSHPVNLTLSA 480
421 LRRSANSAGGVAISFSLTAHSGNYICTADNGFGPQRKAVSLITVPVSHPVNLTLSA 480
481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
481 EALTTEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
541 CTADNGFGPQRSEVSLFVTVPSRPILTLRPRAQAVVGDLLLELHCEAPRGSPILYWF 600
541 CTADNGFGPQRSEVSLFVTVPSRPILTLRPRAQAVVGDLLLELHCEAPRGSPILYWF 600
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660
601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCANNGLVAQHSDDTISLSVIVPSRPI 660
661 LTRAPRAQAVVGDLLLELHCEALRGSSPILYFHYHEDVTLGKISAPSGGASFNLSLTT 720
661 LTRAPRAQAVVGDLLLELHCEALRGSSPILYFHYHEDVTLGKISAPSGGASFNLSLTT 720
721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRGP 780
721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRGP 780
781 LILYRFFHEDVTLGNRSSPGGASLNLSLTAHSGNYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRGP 840
781 LILYRFFHEDVTLGNRSSPGGASLNLSLTAHSGNYSCDADNGLEAQRSEMTLKVAVPVSRPVLTLRAPGTHAAVGDLLLELHCEALRGP 840
841 TANRSGPFATGAGGLTLAGLAAGALLYCNLSKAGKPKASDPARSPSDSDSQEPYH 900
841 TANRSGPFATGAGGLTLAGLAAGALLYCNLSKAGKPKASDPARSPSDSDSQEPYH 900
901 NVPAWELQPVYTNANPRGENVYSEVRIIOEKKHVAASDPRLHNRKSGPIIYSEVKVA 960
901 NVPAWELQPVYTNANPRGENVYSEVRIIOEKKHVAASDPRLHNRKSGPIIYSEVKVA 960
961 STPVSGSLFLASSAPHR 977
961 STPVSGSLFLASSAPHR 977

RESULT 2
Q8NF56 PRELIMINARY; PRT; 437 AA.
ID Q8NF56 Q8NF56;
AC Q8NF56;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE FLJ00333 protein (Fragment).
GN Name=FLJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Iakano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 3.

DR PROSITE; PS0835; IG-LIKE; 3.
FT NON TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 41.2%; Score 403; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 AQAVVGDLLLELHCEAPRGSPILYFHYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSC 634
Db 35 AQAVVGDLLLELHCEAPRGSPILYFHYHEDVTLGSSAPSGGEASFNLSLTAHSGNYSC 94
QY 635 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 694
Db 95 EANNGLVAQHSDDTISLSVIVPSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 154
QY 695 HEDVTLGKISAPSGGASFNLSLTTTSHSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVL 754
Db 155 HEDVTLGKISAPSGGASFNLSLTTTSHSGIYSCDADNGLEAQRSEMTLKVAVPVSRPVL 214
QY 755 LTRAPGTHAAVGDLLLELHCEALRGSPILYFHYHEDVTLGKISAPSGGASFNLSLTAHSG 814
Db 215 LTRAPGTHAAVGDLLLELHCEALRGSPILYFHYHEDVTLGKISAPSGGASFNLSLTAHSG 274
QY 815 GNYSCDADNGLEAQRSEMTLKVAVPVSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 874
Db 275 GNYSCDADNGLEAQRSEMTLKVAVPVSRPILTLRAPGTHAAVGDLLLELHCEALRGSPILYWF 334
QY 875 RKAGRKPAASPPASPSDSQSEPTYNVPAWELQPVYTNANPRGENVYSEVRIIOEKK 934
Db 335 RKAGRKPAASPPASPSDSQSEPTYNVPAWELQPVYTNANPRGENVYSEVRIIOEKK 394
QY 935 KHAVASDPRLHNRKSGPIIYSEVKVASTPVSGSLFLASSAPHR 977
Db 395 KHAVASDPRLHNRKSGPIIYSEVKVASTPVSGSLFLASSAPHR 437

RESULT 3
Q6UY46 PRELIMINARY; PRT; 124 AA.
ID Q6UY46 Q6UY46;
AC Q6UY46;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE IRTA2.
GN ORENAMES=UNQ503;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358085; AA088452.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG-LIKE; 1.
SQ SEQUENCE 124 AA; 14080 MW; D7915849A385455D CRC64;
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Query Match      10.4%; Score 102; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPMTTTFQGERVLTCKGPRFYSPQTKWYHR 60
DB 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPMTTTFQGERVLTCKGPRFYSPQTKWYHR 60

QY 61 YLGKEILRETPDNILEVQESGEYRCQAQCSPLSSPVHLDFSS 102
DB 61 YLGKEILRETPDNILEVQESGEYRCQAQCSPLSSPVHLDFSS 102

RESULT 4
AAQ88452 PRELIMINARY; PRT; 124 AA.
AC AAQ88452;
DT 02-WAR-2004 (TREMBLrel. 27, Created)
DT 02-WAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-WAR-2004 (TREMBLrel. 27, Last annotation update)
DE IRTA2.
GN UNQ503.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358085; AAQ88452.1; -.
SQ SEQUENCE 124 AA; 14080 MW; D7915849A385455D CRC64;

Query Match      10.4%; Score 102; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPMTTTFQGERVLTCKGPRFYSPQTKWYHR 60
DB 1 MLLWILLVLAPVSGQFARTPRPIIFLOPPMTTTFQGERVLTCKGPRFYSPQTKWYHR 60

QY 61 YLGKEILRETPDNILEVQESGEYRCQAQCSPLSSPVHLDFSS 102
DB 61 YLGKEILRETPDNILEVQESGEYRCQAQCSPLSSPVHLDFSS 102

RESULT 5
Q9BZ14 PRELIMINARY; PRT; 144 AA.
AC Q9BZ14;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1c.
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
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RX MEDLINE=21092675; PubMed=11162587;
RA Xu M., Zhao R., Zhao Z.J.;
RT "Molecular Cloning and Characterization of SPAP1, an Inhibitory
RT Receptor.";
RL Biochem. Biophys. Res. Commun. 280:768-775(2001).
DR EMBL; AF319440; AAK01404.1; -.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 144 AA; 15373 MW; D03F859338237CA5 CRC64;

Query Match      2.4%; Score 23; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAEHSGNYSCEANNGL 640
DB 99 ASFNLSLTAEHSGNYSCEANNGL 121

RESULT 6
Q9BZ15 PRELIMINARY; PRT; 192 AA.
AC Q9BZ15;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1b.
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=21092675; PubMed=11162587;
RA Xu M., Zhao R., Zhao Z.J.;
RT "Molecular Cloning and Characterization of SPAP1, an Inhibitory
RT Receptor.";
RL Biochem. Biophys. Res. Commun. 280:768-775(2001).
DR EMBL; AF319439; AAK01403.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0007267; P:cell-cell signaling; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 192 AA; 20680 MW; C9962BBB4B15B08D CRC64;

Query Match      2.4%; Score 23; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAEHSGNYSCEANNGL 640
DB 99 ASFNLSLTAEHSGNYSCEANNGL 121

RESULT 7
Q9BZ16 PRELIMINARY; PRT; 255 AA.
AC Q9BZ16;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 1a (IFGP4).
GN Name=SPAP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092675; PubMed=11162587;
RA Xu M., Zhao R., Zhao Z.J.;
RT "Molecular Cloning and Characterization of SPAP1, an Inhibitory
RL Receptor.";
RL Biochem. Biophys. Res. Commun. 280:768-775(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Tonsil;
RX MEDLINE=22033006; PubMed=12037601;
RA Guseinikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.I., Taranin A.V.;
RT "A family of highly diverse human and mouse genes structurally links
RL leukocyte FcR, gp42 and PECAM-1.";
RL Immunogenetics 54:87-95(2002).
DR EMBL; AF319438; AAK01402.1; -.
DR EMBL; AF390037; AAM12152.1; -.
DR PIR; JC7593; JC7593.
DR GO; GO:0016021; C:Integral to membrane; NAS.
DR GO; GO:0005070; F:SH3/SH2 adaptor protein activity; IPI.
DR GO; GO:0007267; P:Cell-cell signaling; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 255 AA; 27546 MW; 82556447FB6BAB14 CRC64;

Query Match 2.4%; Score 23; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANGL 640
Db 99 ASFNLSLTAEHSGNSYSCEANGL 121

RESULT 8
Q96LA5 PRELIMINARY; PRT; 508 AA.
ID Q96LA5
AC Q96LA5 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fc receptor-like protein 2 (FCRH2).
GN Name=FCRH2; ORFNames=UNQ9236;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RL B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358130; AAQ8497.1; -.
DR EMBL; AY358130; AAQ8497.1; -.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 2.4%; Score 23; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANGL 640
Db 352 ASFNLSLTAEHSGNSYSCEANGL 374

RESULT 10
Q96F30 PRELIMINARY; PRT; 639 AA.
ID Q96F30
AC Q96F30
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Query Match 2.4%; Score 23; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANGL 640
Db 352 ASFNLSLTAEHSGNSYSCEANGL 374

RESULT 9
AAQ88497 PRELIMINARY; PRT; 508 AA.
ID AAQ88497
AC AAQ88497
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE FCRH2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358130; AAQ8497.1; -.
DR EMBL; AY358130; AAQ8497.1; -.
SQ SEQUENCE 508 AA; 55541 MW; 9AB30E0411B41EDC CRC64;

Query Match 2.4%; Score 23; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 618 ASFNLSLTAEHSGNSYSCEANGL 640
Db 352 ASFNLSLTAEHSGNSYSCEANGL 374

RESULT 10
Q96F30 PRELIMINARY; PRT; 639 AA.
ID Q96F30
AC Q96F30
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2b.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN  SEQUENCE FROM N.A.
RP  Xu M.-J., Zhao R., Zhao Z.J.;
RA  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AF416902; AAL13291.1; -.
DR  HSSP; P12319; 1F2Q.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003598; Ig c2.
DR  InterPro; IPR002052; N6_Mtase.
DR  Pfam; PF00047; Ig; 3.
DR  SMART; SM00408; IGC2; 1.
DR  PROSITE; PS50835; IG_LIKE; 5.
DR  PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ  SEQUENCE 639 AA; 69928 MW; DEAD7AD4B64CA984 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 340 ASFNLSLTAHSGNYSC 356
|||||

RESULT 11
ID Q96LA4 PRELIMINARY; PRT; 734 AA.
AC Q96LA4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fc receptor-like protein 3.
GN Name=FCRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777 (2001).
DR EMBL; AY043466; AAK9179.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 435 ASFNLSLTAHSGNYSC 451
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RESULT 12
ID Q96P31 PRELIMINARY; PRT; 734 AA.
AC Q96P31;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FcRH3 protein.

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DE SH2 domain-containing phosphatase anchor protein 2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416901; AAL13290.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 734 AA; 80855 MW; B3411B73A35EC668 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 435 ASFNLSLTAHSGNYSC 451
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RESULT 13
ID Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao R., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416903; AAL13292.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 740 AA; 81440 MW; 038AFA83A2909E46 CRC64;

Query Match 1.7%; Score 17; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 618 ASFNLSLTAHSGNYSC 634
Db 441 ASFNLSLTAHSGNYSC 457
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RESULT 14
ID Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FCRH3 protein.

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RA Sudo H., Hosoiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibaishi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T., Kusano J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mueshino K., Yuuki H., Onima A., Sasaki N., Aotsuka S.,
RA Yoshinaka Y., Matsunawa H., Ichihara T., Shionata N., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyanama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Tozishima-Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamaeshita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA "Complete sequencing and characterization of 21,243 full-length human
RA cDNAs.";
RT Nat. Genet. 36:40-45(2004).
RT EMBL; AK096690; BAC04842.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_Like; 3.
KW Receptor.
SQ SEQUENCE 366 AA; 40434 MW; 6F79D0F9EBD52AE0 CRC64;

Query Match 1.5%; Score 15; DB 2; Length 366;
Best Local Similarity 100.0%; E-Value 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 704 SAPSGGGASFNLSLT 718
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DB 253 SAPSGGGASFNLSLT 267
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Search completed: November 18, 2004, 13:05:01
Job time : 212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 12:53:38 ; Search time 161 Seconds
(without alignments)

2176.885 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977

Sequence: 1 MLWVILLVLPVSGGFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	977	100.0	977	4	AAB82315 Human imm
2	977	100.0	977	7	ADM35237 Human LY1
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4	746	76.4	759	4	AAB82313 Human imm
5	746	76.4	759	7	ADM35235 Human LY1
6	560	57.3	592	4	AAB82314 Human imm
7	560	57.3	592	7	ADM35236 Human LY1
8	194	19.9	222	5	ABP69283 Human pol
9	166	17.0	268	7	ADE08350 Novel pro
10	102	10.4	124	3	RAY66661 Membrane-
11	102	10.4	124	4	AAB65184 Human PRO
12	102	10.4	124	6	ABU57999 Human PRO
13	102	10.4	124	6	ABU5077 Novel hum
14	102	10.4	124	6	ABU82589 Human sec
15	102	10.4	124	6	ABU60508 Human sec
16	102	10.4	124	6	ABU13890 Human PRO
17	102	10.4	124	6	ABU72475 Novel hum
18	102	10.4	124	6	ABP97214 Tumour-as
19	102	10.4	124	6	ABU59224 Human sec
20	102	10.4	124	6	ABO25921 Human PRO
21	102	10.4	124	6	ABU58930 Human sec
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23	102	10.4	124	6	ABU59373 Novel hum
24	102	10.4	124	6	ABU92139 Novel hum
25	102	10.4	124	6	ABU10845 Human PRO

26	102	10.4	124	6	ABU81597	Abu81597 Novel hum
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28	102	10.4	124	6	ABO34050	AbO34050 Human PRO
29	102	10.4	124	6	ADA37657	Ada37657 Human sec
30	102	10.4	124	6	ADA211343	Ada211343 Human sec
31	102	10.4	124	6	ADA10130	Ada10130 Human sec
32	102	10.4	124	6	ADA17674	Ada17674 Human PRO
33	102	10.4	124	6	ADA27782	Ada27782 Human sec
34	102	10.4	124	6	ADA94362	Ada94362 Human sec
35	102	10.4	124	6	ADA38587	Ada38587 Human sec
36	102	10.4	124	6	ADA92708	Ada92708 Human sec
37	102	10.4	124	6	ABO53136	AbO53136 Human sec
38	102	10.4	124	7	ADA22269	Ada22269 Human sec
39	102	10.4	124	7	ABO22506	AbO22506 Human sec
40	102	10.4	124	7	ADA06435	Ada06435 Human sec
41	102	10.4	124	7	ADA39128	Ada39128 Human sec
42	102	10.4	124	7	ADB96154	AdB96154 Human PRO
43	102	10.4	124	7	ADC57626	AdC57626 Human PRO
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45	102	10.4	124	7	ADC11857	AdC11857 Human sec

ALIGNMENTS

RESULT 1
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ID AAB82315 standard; protein; 977 AA.
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XX AAB82315;
AC
XX
DT 23-JUL-2001 (first entry)
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DE Human immunoglobulin receptor isoform IRTA2c.
XX
KW Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2c; human; immunoglobulin receptor; FC receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT Protein /label= Signal_peptide
FT Protein /label= Mature_protein
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FT Binding-site 899..902
FT Binding-site /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT Binding-site 924..927
FT Binding-site /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT Binding-site 954..957

FT /note= "putative consensus Src-homology 2 (SH2) binding
 FT domain"
 XX
 PN WO200138490-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-US032403.
 XX
 PR 29-NOV-1999; 95US-0168151P.
 XX
 PA (UTCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Daila-Favera R;
 XX
 DR WPI; 2001-355921/37.
 XX
 DR N-PSDB; AAF30952.
 XX
 XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
 PT Translocation Associated proteins, used to treat B cell malignancies
 PT including lymphomas and multiple myeloma.
 XX
 PS Claim 3; Fig 18B-1-18B-2; 72pp; English.
 XX
 CC The present sequence is that of the novel human immunoglobulin receptor,
 CC immunoglobulin superfamily receptor translocation associated protein
 CC isoform 2c (IRTA2c), an FC receptor involved in the pathogenesis of
 CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
 CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
 CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
 CC members of a novel subfamily of related receptors within the
 CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
 CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314).
 CC IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein.
 CC Each SH2 binding site agrees with the immune receptor tyrosine-based
 CC inhibition motif (ITIM) consensus and is encoded by a separate exon. The
 CC IRTA genes display a specific pattern of expression in mature B cells,
 CC IRTA2 is expressed in GC centrocytes and in perifollicular cells, which
 CC may include immunoblasts and memory cells. The invention provides IRTA
 CC nucleic acids and proteins, and antibodies directed to epitopes of IRTA
 CC proteins. Methods are claimed for: detecting a B cell malignancy
 CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
 CC that specifically hybridizes with a unique sequence of human IRTA1-5; and
 CC treating a subject having a B cell cancer by administering an anti-IRTA
 CC antibody or an antisense oligonucleotide that specifically hybridizes to
 CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
 CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
 CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
 CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
 CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
 CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
 CC Hodgkin's lymphoma
 XX
 SQ Sequence 977 AA;

Query Match 100.0%; Score 977; DB 4; Length 977;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPPTVFOGERVTLTCKGRFYSPOKTKVYR 60
 QY 61 YLGEKILRETPDNIIEVQSGEYRCQAQGSPLSPVHLDFSSALLIQAPLSVFEGDSV 120
 DB 61 YLGEKILRETPDNIIEVQSGEYRCQAQGSPLSPVHLDFSSALLIQAPLSVFEGDSV 120
 QY 121 LCRKAKEVTLNNTYKNDNLVAFUNKRTDPhiPHACLKONGAYRCTGYKESCCPVSSNT 180
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 DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPSWIQVOIPASHPVLTLSPEKALNFE 300
 QY 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTSTNSGNYICTADNG 360
 DB 301 GTKVTLHCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTSTNSGNYICTADNG 360
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 DB 361 LGAKPSKAVLSLVTVPVSHPVNLSSPEDLIFECAKVTLHCEAQRGSPIILYQFHEDAA 420
 QY 421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
 DB 421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
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 DB 541 CTADNGFGPQRSEVVSFLVTVPVSRPIILTLRVPRAAQVVGDLLELHCEAPRSGSPPILYWF 600
 QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLVIIVPSRPI 660
 DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLVIIVPSRPI 660
 QY 661 LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTT 720
 DB 661 LTFRAPRAQAVVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGGASFNLSLTT 720
 QY 721 HSGIYSCDADNGLQORSEMVTLVAVVPSRPIILTRAPGTHAAVGDLELHCEALRGSP 780
 DB 721 HSGIYSCDADNGLQORSEMVTLVAVVPSRPIILTRAPGTHAAVGDLELHCEALRGSP 780
 QY 781 LLYLFFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGAQRSETVLYITGL 840
 DB 781 LLYLFFHEDVTLGNRSSPSGGASLNLSTAEHSGNYSCEADNGLGAQRSETVLYITGL 840
 QY 841 TANRSGPFATGVAGGLSTAGLAAGALLYLWLSKAGRKSPADPARSPSDSDSQEPTYH 900
 DB 841 TANRSGPFATGVAGGLSTAGLAAGALLYLWLSKAGRKSPADPARSPSDSDSQEPTYH 900
 QY 901 NVPAMEELQPVVTNANPRGENVVYSEVRIIOBKKHAVASDPRLRNKGSPIIYSEVKA 960
 DB 901 NVPAMEELQPVVTNANPRGENVVYSEVRIIOBKKHAVASDPRLRNKGSPIIYSEVKA 960
 QY 961 STPVSGSLFLASSAPHR 977
 DB 961 STPVSGSLFLASSAPHR 977

RESULT 2
 ADM35237
 ID ADM35237 standard; protein; 977 AA.
 XX
 AC ADM35237;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human LY1448P cancer related protein for cancer detection method.
 XX
 KW cytostatic; T-cell vaccine; detection; cancer;
 KW chronic lymphocytic leukemia.
 XX
 OS Homo sapiens.
 XX
 FN WO2003077836-A2.
 XX
 PD 25-SEP-2003.

XX 06-NOV-2002; 2002WO-US035728.
XX 06-NOV-2001; 2001US-00040862.
XX 23-MAY-2002; 2002US-00154884.
XX (CORI-) CORIXA CORP.
XX Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX
XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.
XX
XX Disclosure; SEQ ID NO 10462; 419pp; English.
XX
XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX protein used in the method of the invention.
XX
XX Sequence 977 AA;
XX
XX Query Match 100.0%; Score 977; DB 7; Length 977;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60
XX 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTVFQGERVTLCKGFRFYSPQTKWYHR 60
XX
XX 61 YLGEILLRETPDNLVEQSEGEVCECOAGGSLPSVHLDPSASLILOAPLSVPEGDSVV 120
XX 61 YLGEILLRETPDNLVEQSEGEVCECOAGGSLPSVHLDPSASLILOAPLSVPEGDSVV 120
XX
XX 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPIHACLKONGAYRCTGYKESCCPVSSNT 180
XX 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPIHACLKONGAYRCTGYKESCCPVSSNT 180
XX
XX 181 VKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLWS 240
XX 181 VKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLWS 240
XX
XX 241 LSPNFQITAMWSKDSGFVCKAAWPHSVISDSRPSWIOQVIPASHPVLTLSPEKALNPE 300
XX 241 LSPNFQITAMWSKDSGFVCKAAWPHSVISDSRPSWIOQVIPASHPVLTLSPEKALNPE 300
XX
XX 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTTENSNNYCTADNG 360
XX 301 GTKVTLHCETQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTTENSNNYCTADNG 360
XX
XX 361 LGAKPSKAVSLSVTPVSHVNLSSPEDLIFECAKVTLHCEAORGSLPILYOPHHEDAA 420
XX 361 LGAKPSKAVSLSVTPVSHVNLSSPEDLIFECAKVTLHCEAORGSLPILYOPHHEDAA 420
XX
XX 421 LERRANSAGGVAISFSLTAHSGNNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
XX 421 LERRANSAGGVAISFSLTAHSGNNYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
XX
XX 481 BALTFEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540

DB 481 EALTPEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTECHSGNY 540
QY 541 CTADNGFGPQRSSEVVSFLVTVPSRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSSEVVSFLVTVPSRPILTLRVPRAQAVVGDLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTTE 720
QY 721 HSGIYSCADNGLEAQRSEWMTLKVAVPSRPVTLTRAPGTHAAVGDLELHCEALRGSP 780
DB 721 HSGIYSCADNGLEAQRSEWMTLKVAVPSRPVTLTRAPGTHAAVGDLELHCEALRGSP 780
QY 781 LILYRPFHEDVTLGNRRSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVTLIITGL 840
DB 781 LILYRPFHEDVTLGNRRSPSGGASLNLSLTAHSGNYSCEADNGLGAQRSETVTLIITGL 840
QY 841 TANRSGPATGVAGGLLSIAGLAAGALLYLWLSRKAGKPKASDPARSPSDSDSOEPTYH 900
DB 841 TANRSGPATGVAGGLLSIAGLAAGALLYLWLSRKAGKPKASDPARSPSDSDSOEPTYH 900
QY 901 NYPAMEELQPVYTNANPRGENVYSEVRIOEKKKHAVASDPHRHNRKSGSPIIYSEVKVA 960
DB 901 NYPAMEELQPVYTNANPRGENVYSEVRIOEKKKHAVASDPHRHNRKSGSPIIYSEVKVA 960
QY 961 STPVSGSLFLASSAPHR 977
DB 961 STPVSGSLFLASSAPHR 977

RESULT 3
ABP97215
ID ABP97215 standard; protein; 977 AA.
XX
XX AC ABP97215;
XX XX
XX DT 01-JUL-2003 (first entry)
XX
XX DE Tumour-associated antigenic target protein TAT374 SEQ ID NO:97.
XX XX
XX KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
XX cancer.
XX OS Homo sapiens.
XX
XX PN WO2003024392-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 11-SEP-2002; 2002WO-US028859.
XX
XX PR 18-SEP-2001; 2001US-0323268P.
XX PR 19-OCT-2001; 2001US-0339227P.
XX PR 07-NOV-2001; 2001US-0338827P.
XX PR 20-NOV-2001; 2001US-0331906P.
XX PR 02-JAN-2002; 2002US-0345444P.
XX PR 03-APR-2002; 2002US-0369724P.
XX PR 19-AUG-2002; 2002US-0404809P.
XX
XX (GETH) GENENTECH INC.
XX
XX PI Prantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;
XX PI Williams PW, Wu TD, Zhang Z;
XX
XX WPI; 2003-354551/33.
XX DR N-PSDB; ACC49533.
XX
XX

PT New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.
PS Claim 2; Fig 97; 285pp; English.
XX
CC ACC49493 to ACC49552 encode the human tumour-associated antigenic target
CC (TAT) proteins given in AB997175 to AB997234. The present invention
CC describes an isolated antibody that binds to a polypeptide having at
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC sequences (S1), given in AB997175 to AB997234, comprising (S1), lacking
CC its associated signal peptide, encoded by any of the 60 2000-3000 base
CC pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer
XX
SQ Sequence 977 AA;

Query Match 80.7%; Score 788; DB 6; Length 977;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTICKGRFFYSPOKTKVHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVLTICKGRFFYSPOKTKVHR 60

QY 61 YLGKILRETPDNILEVQESGEYRCQAQCSPLSPVHLDFSSASLILQAPLSVFEQSVV 120
DB 61 YLGKILRETPDNILEVQESGEYRCQAQCSPLSPVHLDFSSASLILQAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTYKNDNLVAFUNKRTDPhiPHACLKONGAVRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTYKNDNLVAFUNKRTDPhiPHACLKONGAVRCTGYKESCCPVSSNT 180

QY 181 VKIQOEPTFPVLRASSFQPIGNSPVLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240
DB 181 VKIQOEPTFPVLRASSFQPIGNSPVLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240

QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSRSTQVQIPASHVPLTILSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSRSTQVQIPASHVPLTILSPKALNFE 300

QY 301 GPKVTLHCETQDSDSLRTLYRFYHEGVPLRHKSVCRCERGISFSFLTENSNGNYCTADNG 360
DB 301 GPKVTLHCETQDSDSLRTLYRFYHEGVPLRHKSVCRCERGISFSFLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420
DB 361 LGAKPSKAVSLSVTVVPSHPVLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQPHHDA 420

QY 421 LERRSANGAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERRSANGAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480

QY 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTPEGATVTLHCEVQRGSQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFQPSRSEVSVLVTVVPSRPILTLPVRAQAVGVDLLHCEAPRGSPILYWF 600
DB 541 CTADNGFQPSRSEVSVLVTVVPSRPILTLPVRAQAVGVDLLHCEAPRGSPILYWF 600

QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSIIVPSRP 660
DB 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSIIVPSRP 660

QY 661 LTFRAPRAQAVGVDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
DB 661 LTFRAPRAQAVGVDLLHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720

QY 721 HSGIYSCADNGLGAQRSEWTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780
DB 721 HSGIYSCADNGLGAQRSEWTLKVAVPVSRPVLTLRAPGTHAAVGDLLLEHCEALRGSP 780

QY 781 LILYRFFHEDVTLGNRSSPSSGASLNLSLTAEHSGNYSCEADNGLGAQRSEWTLITGL 840
DB 781 LILYRFFHEDVTLGNRSSPSSGASLNLSLTAEHSGNYSCEADNGLGAQRSEWTLITGL 840

QY 841 TANRSQPFATGVAGLLSLTAGLAAGALLYCWLRRKAGKPKASDPARSP 889
DB 841 TANRSQPFATGVAGLLSLTAGLAAGALLYCWLRRKAGKPKASDPARSP 889

RESULT 4
AAB82313
ID AAB82313 standard; protein; 759 AA.
XX
AC AAB82313;
XX
XX 23-JUL-2001 (first entry)
XX
XX Human immunoglobulin receptor isoform IRTA2a.
DE
XX Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..15
FT /label= Signal_peptide
FT Protein 16..759
FT /label= Mature_protein
FT Modified-site 132..134
FT /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT /note= "Asn is N-glycosylated"
FT Modified-site 621..623
FT /note= "Asn is N-glycosylated"
FT Modified-site 631..633
FT /note= "Asn is N-glycosylated"
FT Modified-site 714..716
FT /note= "Asn is N-glycosylated"
XX
XX MO200138490-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-US032403.
XX
XX 29-NOV-1999; 99US-0168151P.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Dalla-Pavera R;
XX
XX WPI; 2001-355921/37.
XX N-PSDB; AAF30950.
XX
XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX
XX Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX
XX The present sequence is that of the novel human immunoglobulin receptor,
XX immunoglobulin superfamily receptor translocation associated protein
XX isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of
XX lymphoma and melanoma. Efforts to identify genes involved in chromosomal
XX aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
XX led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
XX members of a novel subfamily of related receptors within the

immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315). IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue 560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at residue 746 and extends for a further 231 residues. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to an epitope of an IRTA protein. Methods are claimed for: detecting a B cell malignancy comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma

XX
SQ Sequence 759 AA;

Query Match 76.4%; Score 746; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Qy 61 YLGEKILRETPDNILEVQESGEYRCQAGSPLSPVHLDFSSASLILOAPLSVFEQDSVV 120
Db 61 YLGEKILRETPDNILEVQESGEYRCQAGSPLSPVHLDFSSASLILOAPLSVFEQDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKXNDVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKXNDVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVEEFTFPVLRASSFPQISGNPVTLTCTQSLERSDVPLRFRFFDDQTLGLGWS 240
Db 181 VKIQVEEFTFPVLRASSFPQISGNPVTLTCTQSLERSDVPLRFRFFDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFVWCXAAITMPSVSDSPRSWIQVQIPASHVPLTILSPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFVWCXAAITMPSVSDSPRSWIQVQIPASHVPLTILSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVCERCASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVCERCASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTVPSGHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTVPSGHPVNLSSPEDLIPEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRANSAGGVAISFSLTAHSGNYCTADNGPQSKAVSLITVPVSHVPLTILSSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYCTADNGPQSKAVSLITVPVSHVPLTILSSA 480
Qy 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
Db 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNGNY 540
Qy 541 CTADNGFGPQRESEVSLFVTVPSRPILTILRVPRQAQVVGDLLELHCEAPGSPILYWF 600
Db 541 CTADNGFGPQRESEVSLFVTVPSRPILTILRVPRQAQVVGDLLELHCEAPGSPILYWF 600
Qy 601 YHEDVTLGSSSAPSGGEAFNLSTAHSNGYSCANNGLVAQHSDDTISLSVIVPSRPI 660
Db 601 YHEDVTLGSSSAPSGGEAFNLSTAHSNGYSCANNGLVAQHSDDTISLSVIVPSRPI 660

Qy 661 LTFRAPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDILLEHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTTE 720
Qy 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746
Db 721 HSGIYSCDADNGLEAQRSEMVTLKVA 746

RESULT 5

ADM35235
ID ADM35235 standard; protein; 759 AA.
AC ADM35235;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related protein for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
DR
XX
PT Detecting cancer in a patient comprises contacting a biological sample from the patient with a binding agent that binds to a cancer-associated polypeptide and comparing the amount of polypeptide to a predetermined cutoff value.
PT
PS Disclosure; SEQ ID NO 10460; 419pp; English.
XX

The invention relates to a method of detecting (M1) cancer in a patient by: (i) contacting a biological sample from the patient with an agent that binds to any of three polypeptides given in the specification; (ii) detecting in a sample an amount of the peptide that binds to the binding agent; and (iii) comparing the amount of polypeptide present in the patient's sample to a predetermined cutoff value. The specification also discloses a separate method for detecting (M2) cancer in a patient by a method similar to M1, except that the detection agent is an oligonucleotide that binds to any of three polynucleotides given in the specification. M1 and M2 are useful for detecting the presence of cancer in a patient, especially chronic lymphocytic leukemia. The applicants have identified specific human polypeptides overexpressed in one or more types of hematological malignancies. This sequence corresponds to a protein used in the method of the invention.

Sequence 759 AA;

Query Match 76.4%; Score 746; DB 7; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVAPVSGQARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Qy 61 YLGEKILRETPDNILEVQESGEYRCQAGSPLSPVHLDFSSASLILOAPLSVFEQDSVV 120

Db 61 YLKEILLRETPDNILEVQESGEGYRCAQAGSPVHLDFFSASLILQAPLSVEFGDSVV 120
 QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDFHPIHACLNKNGAYRCTGYKESCCPVSSNT 180
 Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDFHPIHACLNKNGAYRCTGYKESCCPVSSNT 180
 QY 181 VKIQVQEPPTRVPLRASSFQPIISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
 Db 181 VKIQVQEPPTRVPLRASSFQPIISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
 QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
 Db 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300
 QY 301 GTKVTLHCETQDSDRLTYRFYHGVPLRHKSVCRCERGASISFSLTTTNSGNYICTADNG 360
 Db 301 GTKVTLHCETQDSDRLTYRFYHGVPLRHKSVCRCERGASISFSLTTTNSGNYICTADNG 360
 QY 361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 420
 Db 361 LGAKPSKAVSLSVTVPSHVPVNLSSPEDLIFEGAKVTLHCEAORGSLPILYQPHHEDAA 420
 QY 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTVPSHVPVLTLSA 480
 Db 421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSVTVPSHVPVLTLSA 480
 QY 481 EALTTEGATVTLHCEVQSGSPOLLQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
 Db 481 EALTTEGATVTLHCEVQSGSPOLLQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
 QY 541 CTADNGFGPQSEVSVLFTVPSRPILTLPVRAQAVGVGDLLELHCEAPRGSPILYWF 600
 Db 541 CTADNGFGPQSEVSVLFTVPSRPILTLPVRAQAVGVGDLLELHCEAPRGSPILYWF 600
 QY 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDISLSVIVPSRPI 660
 Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDDISLSVIVPSRPI 660
 QY 661 LTFRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
 Db 661 LTFRAPRAQAVGDLLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLTT 720
 QY 721 HSGIYSCDADNGLEAQRSEMTLKV 746
 Db 721 HSGIYSCDADNGLEAQRSEMTLKV 746

RESULT 6 AAB82314

ID AAB82314 standard; protein; 592 AA.

XX AC AAB82314;

XX DT 23-JUL-2001 (first entry)

XX DE Human immunoglobulin receptor isoform IRTA2b.

XX KW Immunoglobulin superfamily receptor translocation associated; IRTA;

XX KW IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;

XX KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..15

FT Protein /label= Signal_peptide

FT Protein 16..592

FT Protein /label= Mature_protein

FT Modified-site 132..134

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 383..385

XX /note= "Asn is N-glycosylated"

PN W0200138490-A2.
 XX 31-MAY-2001
 XX 28-NOV-2000; 2000NO-US032403.
 XX 29-NOV-1999; 99US-0168151P.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX Dalla-Favera R;
 XX WPI; 2001-355921/37.
 XX N-PSDB; AAF30951.

XX New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
 PT Translocation Associated proteins, used to treat B cell malignancies
 PT including lymphomas and multiple myeloma.

XX Claim 3; Fig 18B-1-18B-2; 72pp; English.

XX The present sequence is that of the novel human immunoglobulin receptor,
 CC immunoglobulin superfamily receptor translocation associated protein
 CC isoform 2b (IRTA2b), an Fc receptor involved in the pathogenesis of
 CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
 CC aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma
 CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
 CC members of a novel subfamily of related receptors within the
 CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
 CC isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).
 CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at
 CC residue 560, extending for a further 32 residues, whose hydrophobicity
 CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes
 CC display a specific pattern of expression in mature B cells. IRTA2 is
 CC expressed in GC centrocytes and in perifollicular cells, which may
 CC include immunoblasts and memory cells. The invention provides IRTA
 CC nucleic acids and proteins, and antibodies directed to an epitope of an
 CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
 CC comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule
 CC that specifically hybridises with a unique sequence of human IRTA1-5; and
 CC treating a subject having a B cell cancer by administering an anti-IRTA
 CC antibody or an antisense oligonucleotide that specifically hybridises to
 CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
 CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
 CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
 CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
 CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
 CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
 CC Hodgkin's lymphoma

XX Sequence 592 AA;

Query Match 57.3%; Score 560; DB 4; Length 592;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLAPVSGQPARTPRPIIFLOPPWTTVQGERVTLTKGFRFPYSPQTKWYHR 60
 Db 1 MLLWILLVLAPVSGQPARTPRPIIFLOPPWTTVQGERVTLTKGFRFPYSPQTKWYHR 60
 QY 61 YLKGKILRETPDNILEVQESGEGYRCAQAGSPVHLDFFSASLILQAPLSVEFGDSVV 120
 Db 61 YLKGKILRETPDNILEVQESGEGYRCAQAGSPVHLDFFSASLILQAPLSVEFGDSVV 120
 QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDFHPIHACLNKNGAYRCTGYKESCCPVSSNT 180
 Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTRDFHPIHACLNKNGAYRCTGYKESCCPVSSNT 180
 QY 181 VKIQVQEPPTRVPLRASSFQPIISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
 Db 181 VKIQVQEPPTRVPLRASSFQPIISGNPVTLCETQLSLERSDVPFRFRDDQTLGLGWS 240
 QY 241 LSPNFQITAMWSKDSGFYWCKAATPHSVISDSPRSWIQVOIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTANGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTANGFGPQRSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSLTECHSGNYY 540
Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSLTECHSGNYY 540
Qy 541 CTADNGFGPQRSEVVSFLVFT 560
Db 541 CTADNGFGPQRSEVVSFLVFT 560

RESULT 7

ADM35236
ID ADM35236 standard; protein; 592 AA.

AC ADM35236;

DT 03-JUN-2004 (first entry)

DE Human LY1448P cancer related protein for cancer detection method.

EW cytostatic; T-cell vaccine; detection; cancer;

KW chronic lymphocytic leukemia.

XX Homo sapiens.

OS WO2003077836-A2.

PN 25-SEP-2003.

PD 06-NOV-2002; 2002WO-US035728.

PF 06-NOV-2001; 2001US-00040862.

PR 23-MAY-2002; 2002US-00154884.

XX (CORI-) CORIXA CORP.

XX Gaiger A, Algate PA, Mannion J, Retter M;

XX WPI; 2003-756941/71.

XX Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.

XX Disclosure; SEQ ID NO 10461; 419pp; English.

XX The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more

CC types of hematological malignancies. This sequence corresponds to a
CC protein used in the method of the invention.

XX Sequence 592 AA;

Qy Query Match 57.3%; Score 560; DB 7; Length 592;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLUWVILLVLAPVSGOFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRYSQKTKWYHR 60

Db 1 MLUWVILLVLAPVSGOFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRYSQKTKWYHR 60

Qy 61 YLGEKILRETPDNILLEVQESGEYRCAQGSPLSSPVHLDFSSASLIQAPLVSFEGDSVY 120

Db 61 YLGEKILRETPDNILLEVQESGEYRCAQGSPLSSPVHLDFSSASLIQAPLVSFEGDSVY 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHI PHACLKDNKAYACTGYKESCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPDHI PHACLKDNKAYACTGYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNPVTILTCETQLSLERSDVPFRFRDDQTLGLWS 240

Db 181 VKIQVQEPFTRPVLRASSFPISGNPVTILTCETQLSLERSDVPFRFRDDQTLGLWS 240

Qy 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHHPVLTLSPEKALNFE 300

Db 241 LSPNFOITAMWSKDSGFYWCKAATWPHSVISDSRSMIQVQIPASHHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

Db 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCERGASISFSLTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQRGSLPILYQPHHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSVTPVSHPVLTLSA 480

Qy 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSLTECHSGNYY 540

Db 481 EALTPEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPVGVSFSLTECHSGNYY 540

Qy 541 CTADNGFGPQRSEVVSFLVFT 560

Db 541 CTADNGFGPQRSEVVSFLVFT 560

RESULT 8

ABP69283

ID ABP69283 standard; protein; 222 AA.

XX AC ABP69283;

XX AC ABP69283;

DT 20-JAN-2003 (first entry)

XX Human polypeptide SEQ ID NO 1330.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
CC cell-proliferative disorder; neurodegenerative disease; bacterial;
CC Parkinson's disease; Alzheimer's disease; autoimmune disease;
CC multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
CC arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
CC antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
CC haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
CC antiarthritic.

XX Homo sapiens.

XX WO200270539-A2.

XX

PD 12-SEP-2002.
 XX
 XX 05-MAR-2002; 2002WO-US005095.
 XX
 XX 05-MAR-2001; 2001US-00799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 XX WPI: 2002-759812/82.
 DR N-PSDB; ABZ11500.
 XX
 XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.
 XX
 XX Claim 9; SEQ ID NO 1330; 1012pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP6902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 222 AA;
 SQ
 Query Match 19.9%; Score 194; DB 5; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1e-176;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 268 SVISDPSRWIQVQIPASHPVLTLSPEKALNFEQTKVTLHCETQEDSLRTLYRFYHEGVP 327
 DB 19 SVISDPSRWIQVQIPASHPVLTLSPEKALNFEQTKVTLHCETQEDSLRTLYRFYHEGVP 78
 QY 328 LRHKSVRCRGASISFSLTENSNGNYCTADNGLGAKPSKAVSLVTPVSHPVLTLSPP 387
 DB 79 LRHKSVRCRGASISFSLTENSNGNYCTADNGLGAKPSKAVSLVTPVSHPVLTLSPP 138
 QY 388 EDLIEFGAKVTTLHCAQRGSLPILYQFHEDAALRRRANGAGGVAISFSLTAHSGNYY 447
 DB 139 EDLIEFGAKVTTLHCAQRGSLPILYQFHEDAALRRRANGAGGVAISFSLTAHSGNYY 198
 QY 448 CTADNGFGPQRSKA 461
 DB 199 CTADNGFGPQRSKA 212
 RESULT 9
 ADE08350
 ID ADE08350 standard; protein; 269 AA.
 XX
 AC ADE08350;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #505.
 XX novel gene; novel protein; tissue marker; molecular weight marker;
 KW

XX chromosome marker; genetic disorder.
 XX Unidentified.
 XX WO2003054152-A2.
 XX
 XX 03-JUL-2003.
 XX
 XX 10-DEC-2002; 2002WO-US039555.
 XX
 XX 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 XX WPI: 2003-569235/53.
 DR N-PSDB; ADE07439.
 XX
 XX New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 XX Claim 20; SEQ ID NO 1416; 1177pp; English.
 PS
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 CC
 XX Sequence 268 AA;
 SQ
 Query Match 17.0%; Score 166; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8.1e-150;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 766 GDLELHCEALRGSPILYRFFHEDVTLGNRSPSGGASLNLSTAHSNGVSCADNGL 825
 DB 57 GDLELHCEALRGSPILYRFFHEDVTLGNRSPSGGASLNLSTAHSNGVSCADNGL 116
 QY 826 GAQRSTVTLYITGLTANRSGPFATGVAGLLSIAGLAAGALLXCWLSRKAGRXPASDP 885
 DB 117 GAQRSTVTLYITGLTANRSGPFATGVAGLLSIAGLAAGALLXCWLSRKAGRXPASDP 176
 QY 886 ARSPSDSDSQEPTHYHNPVPAWEELQPYTYTNANRGENVYSEVRIIQ 931
 DB 177 ARSPSDSDSQEPTHYHNPVPAWEELQPYTYTNANRGENVYSEVRIIQ 222
 RESULT 10
 AAY66661
 ID AAY66661 standard; protein; 124 AA.
 XX
 AC AAY66661;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO820.
 XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW


```

XX (GETH ) GENENTECH INC.
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX WPI: 2000-072883/06.
DR N-PSDB; AA264992.
XX Membrane-bound proteins and related nucleotide sequences.
PT Claim 12; Fig 83; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX ligands have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
XX
XX Sequence 124 AA;
XX
XX Query Match 10.4%; Score 102; DB 3; Length 124;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-89;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPMTTTFQGERVLTICKGRFRFYSQTKWYHR 60
XX Db 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPMTTTFQGERVLTICKGRFRFYSQTKWYHR 60
XX
XX QY 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX Db 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX
XX RESULT 11
XX AAB65184
XX ID AAB65184 standard; protein; 124 AA.
XX AC AAB65184;
XX DT 02-APR-2001 (first entry)
XX DE Human PRO820 (UNQ503) protein sequence SEQ ID NO:146.
XX KW Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
XX KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX KW diagnostic assay.
XX OS Homo sapiens.
XX
XX FN WO200073454-A1.
XX PD 07-DEC-2000.
XX PF 30-MAR-2000; 2000WO-US008439.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 07-JUL-1999; 99US-0143048P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 17-AUG-1999; 99US-0149398P.
XX PR 15-SEP-1999; 99WO-US021090.
XX
XX 15-SEP-1999; 99WO-US021547.
XX 08-OCT-1999; 99US-0158663P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI: 2001-032160/04.
XX DR N-PSDB; AAF44138.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 12; Fig 83; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
XX AAB65300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention
XX
XX Sequence 124 AA;
XX
XX Query Match 10.4%; Score 102; DB 4; Length 124;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-89;
XX Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPMTTTFQGERVLTICKGRFRFYSQTKWYHR 60
XX Db 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPMTTTFQGERVLTICKGRFRFYSQTKWYHR 60
XX
XX QY 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX Db 61 YLKGKILRETPDNILEVQESGYRCQAQGSPLSSPVHLDFFS 102
XX
XX RESULT 12
XX AAB65184
XX ID AAB65184 standard; protein; 124 AA.
XX AC AAB65184;
XX DT 14-APR-2003 (first entry)
XX DE Human PRO polypeptide #31.

```


XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0065770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078940P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087753P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088039P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088856P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090245P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
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PR 24-AUG-1998; 98US-0097661P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.

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PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
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PR 08-OCT-1999; 99WO-US021547.
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PR 01-DEC-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030091.
PR 05-JAN-2000; 99WO-US030911.
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PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
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PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLWLWILLVAVSGQFARTPRPIIFLOPPWTTVFQGERVLTICKGFRFYSPOKTKVHR 60

QY 61 YLGKEILRTPDNILEVSGEYRCQAQCSPLSSPVHLDFFS 102
DB 61 YLGKEILRTPDNILEVSGEYRCQAQCSPLSSPVHLDFFS 102

RESULT 13
ABU59077
ID ABU59077 standard; protein; 124 AA.
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AC ABU59077;
XX
DT 28-APR-2003 (first entry)
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DE Novel human secreted or transmembrane protein PRO820.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;

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KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
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PR 18-JUN-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.

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PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
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PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
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PR 22-FEB-2000; 2000WO-US004414.
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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 28-JUL-2000; 2000WO-US020710.
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PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
PA (GETH) GENENTECH INC.
XX
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Perrara N, Fong S, Gerber H, Gerritsen WE, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AJ, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-247083/24.
DR N-PSDB; ABX80219.
DE
XX
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
XX Claim 12; Fig 83; 648pp; English.
PS
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and angiogenesis of this polypeptide are
XX useful for treating cancerous tumors. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 124 AA;

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVLTCKGFRFYSQKTKWYHR 60

QY 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFS 102
DB 61 YLKGKILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFFS 102

RESULT 14
ABU82589
ID ABU82589 standard; protein; 124 AA.
XX
XX AC ABU82589;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO820.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX
XX OS Homo sapiens.
XX
XX PN US2003032023-A1.
XX
XX PD 13-FEB-2003.
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XX PF 14-NOV-2001; 2001US-00990711.
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XX PR 16-JUN-1997; 97US-0049787P.
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XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
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XX PR 20-MAR-1998; 98US-0078910P.
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XX PR 02-JUN-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 03-JUN-1998; 98US-0087759P.
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PR 04-AUG-1998; 98US-0095325P.
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PR 11-AUG-1998; 98US-0096146P.
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PR 16-SEP-1998; 98WO-US013330.
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PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
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Query Match 10.4%; Score 102; DB 6; Length 124;

Best Local Similarity 100.0%; Pred. No. 7.6e-89; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

ABU60508

ID ABU60508 standard; protein; 124 AA.

XX AC ABU60508;

XX DT 01-MAY-2003 (first entry)

XX DE Human secreted/transmembrane protein, #52.

XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX KW diagnostic; therapeutic; gene therapy.

XX OS Homo sapiens.

XX PN US2002160384-A1.

XX PD 31-OCT-2002.

XX PF 14-NOV-2001; 2001US-00925298.

XX PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.

PR 12-NOV-1997; 97US-0065186P.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088023P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 05-JUN-1998; 98US-0088326P.

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PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
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PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 18-JUN-1998; 98US-00899330.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 26-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PSDB; ABX90197.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 83; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 124 AA;

Query Match 10.4%; Score 102; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||
1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
QY 61 YLGKEILRETPDNILEVQSGEYRQAOQSGPLSSPVHLDFFS 102
Db |||||
61 YLGKEILRETPDNILEVQSGEYRQAOQSGPLSSPVHLDFFS 102

Search completed: November 18, 2004, 13:01:27
Job time : 166 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 13:05:09 ; Search time 155 Seconds

(without alignments)
2232.146 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977
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Gapop 60.0 , Gapext 60.0

Searched: 1570615 seqs, 354127592 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	977	100.0	977	15	US-10-057-475B-10461 Sequence 10462, A
3	977	100.0	977	15	US-10-154-884B-10462 Sequence 10462, A
4	977	100.0	977	15	US-10-403-847-9 Sequence 9, Appli
5	977	100.0	977	16	US-10-764-324-10462 Sequence 10462, A
6	788	80.7	977	14	US-10-241-220-97 Sequence 97, Appl
7	746	76.4	759	14	US-10-040-862-10460 Sequence 10460, A
8	746	76.4	759	15	US-10-057-475B-10460 Sequence 10460, A
9	746	76.4	759	15	US-10-154-884B-10460 Sequence 10460, A
10	746	76.4	759	15	US-10-403-847-7 Sequence 7, Appli
11	746	76.4	759	16	US-10-764-324-10460 Sequence 10460, A
12	644	65.9	790	15	US-10-403-847-4 Sequence 4, Appli
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14	560	57.3	592	15	US-10-057-475B-10461	Sequence 10461, A
15	560	57.3	592	15	US-10-154-884B-10461	Sequence 10461, A
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17	560	57.3	592	16	US-10-764-324-10461	Sequence 10461, A
18	281	28.8	317	15	US-10-403-847-2	Sequence 2, Appli
19	246	25.2	438	15	US-10-403-847-6	Sequence 6, Appli
20	151	15.5	152	15	US-10-403-847-10	Sequence 10, Appli
21	113	11.6	113	15	US-10-403-847-139	Sequence 139, App
22	102	10.4	102	15	US-10-403-847-124	Sequence 124, App
23	102	10.4	124	9	US-09-989-723-146	Sequence 146, App
24	102	10.4	124	9	US-09-989-723-146	Sequence 146, App
25	102	10.4	124	9	US-09-989-273-146	Sequence 146, App
26	102	10.4	124	9	US-09-989-727-146	Sequence 146, App
27	102	10.4	124	9	US-09-989-731-146	Sequence 146, App
28	102	10.4	124	9	US-09-989-732-146	Sequence 146, App
29	102	10.4	124	9	US-09-991-073-146	Sequence 146, App
30	102	10.4	124	9	US-09-990-443-146	Sequence 146, App
31	102	10.4	124	9	US-09-991-163-146	Sequence 146, App
32	102	10.4	124	9	US-09-993-604-146	Sequence 146, App
33	102	10.4	124	9	US-09-990-456-146	Sequence 146, App
34	102	10.4	124	9	US-09-989-721-146	Sequence 146, App
35	102	10.4	124	9	US-09-992-598-146	Sequence 146, App
36	102	10.4	124	9	US-09-989-293A-146	Sequence 146, App
37	102	10.4	124	9	US-09-989-735-146	Sequence 146, App
38	102	10.4	124	9	US-09-990-444-146	Sequence 146, App
39	102	10.4	124	9	US-09-991-181-146	Sequence 146, App
40	102	10.4	124	9	US-09-989-730-146	Sequence 146, App
41	102	10.4	124	9	US-09-990-436-146	Sequence 146, App
42	102	10.4	124	9	US-09-993-687-146	Sequence 146, App
43	102	10.4	124	10	US-09-989-734-146	Sequence 146, App
44	102	10.4	124	10	US-09-997-653-146	Sequence 146, App
45	102	10.4	124	10	US-09-989-724-146	Sequence 146, App

ALIGNMENTS

RESULT 1

US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416

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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
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; ORGANISM: Homo sapiens
US-10-040-862-10462

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Db 1 MLLWVILLVAPVSGGFARTPRPIIFLOPPWTTVFGGERVTLTCKGFRFYSPQKTWYHR 60
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RESULT 2
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; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
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; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
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; PRIOR FILING DATE: 2000-08-03
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; NUMBER OF SEQ ID NOS: 10979
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; TYPE: PRT
; ORGANISM: Homo sapiens
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QY 781 LILYRFFHEDVTLGSRSSPGGASNLSTAEHSGNYSCEADNGLGCAQRSETVLYITGL 840
Db 781 LILYRFFHEDVTLGSRSSPGGASNLSTAEHSGNYSCEADNGLGCAQRSETVLYITGL 840
QY 841 TANRSGPFATGVAGGLLSIAGLAAGALLIYCWLSRKAGRKPAASDPARSPSDSQEPTIYH 900
Db 841 TANRSGPFATGVAGGLLSIAGLAAGALLIYCWLSRKAGRKPAASDPARSPSDSQEPTIYH 900
QY 901 NVPAMEELOPVYTNANPRGENVYSEVRITIQEKKHAAVADDPRLRNKGPSPIIYSEVKVA 960
Db 901 NVPAMEELOPVYTNANPRGENVYSEVRITIQEKKHAAVADDPRLRNKGPSPIIYSEVKVA 960
QY 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 4

US-10-403-847-9
; Sequence 9, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; PRIOR FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-9

Query Match 100.0%; Score 977; DB 15; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPQWTVTFQGERVTLTCCKGFREYSPQKTKWYHR 60
Db 1 MLLWVILLVAPVSGQFARTPRPIIFLOPQWTVTFQGERVTLTCCKGFREYSPQKTKWYHR 60
QY 61 YLCKEILRETPDNILEVOESGEYRCAQSPSSPVHLDFFSSASLIQAPLSVFEGDSV 120
Db 61 YLCKEILRETPDNILEVOESGEYRCAQSPSSPVHLDFFSSASLIQAPLSVFEGDSV 120
QY 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRDTFHPHACLKNDGAYRGTGKSCCPVSSNT 180
Db 121 LRCRAAEVTLNNTIYKNDNVLAFLNKRDTFHPHACLKNDGAYRGTGKSCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSPQISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSPQISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240
QY 241 LSNFQITAMWKSQSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNPE 300
Db 241 LSNFQITAMWKSQSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPEKALNPE 300
QY 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVRCEGASISFSLTSTENSGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFVHEGVPLRHKSVRCEGASISFSLTSTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRANSAGGVAISFSLTAHSGNYSCTADNGFGPQSRKAVSLSTVPSHPVLTLSA 480
Db 421 LERRANSAGGVAISFSLTAHSGNYSCTADNGFGPQSRKAVSLSTVPSHPVLTLSA 480
QY 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPFSVGRVSFSFSLTEHSGNY 540
Db 481 EALTTFEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPFSVGRVSFSFSLTEHSGNY 540
QY 541 CTADNGFGPQSRSEVSLFVTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQSRSEVSLFVTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
QY 601 YHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
Db 601 YHEDVTLGSSAPSGEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPVSRI 660
QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGGASFNLSLTTE 720
Db 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYHEDVTLGKISAPSGGGASFNLSLTTE 720
QY 721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRIPLTRAPGTHAAVGDLELHCEALRGSP 780
Db 721 HSGIYSCDADNGLEAQRSEMTLKVAVPVSRIPLTRAPGTHAAVGDLELHCEALRGSP 780
QY 781 LILYRFFHEDVTLGSRSSPGGASNLSTAEHSGNYSCEADNGLGCAQRSETVLYITGL 840
Db 781 LILYRFFHEDVTLGSRSSPGGASNLSTAEHSGNYSCEADNGLGCAQRSETVLYITGL 840
QY 841 TANRSGPFATGVAGGLLSIAGLAAGALLIYCWLSRKAGRKPAASDPARSPSDSQEPTIYH 900
Db 841 TANRSGPFATGVAGGLLSIAGLAAGALLIYCWLSRKAGRKPAASDPARSPSDSQEPTIYH 900
QY 901 NVPAMEELOPVYTNANPRGENVYSEVRITIQEKKHAAVADDPRLRNKGPSPIIYSEVKVA 960
Db 901 NVPAMEELOPVYTNANPRGENVYSEVRITIQEKKHAAVADDPRLRNKGPSPIIYSEVKVA 960
QY 961 STPVSGSLFLASSAPHR 977
Db 961 STPVSGSLFLASSAPHR 977

RESULT 5

US-10-764-324-10462
; Sequence 10462, Application US/10764324
; Publication No. US2004017599A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126

```
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10462
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-10462

Query Match
Best Local Similarity 100.0%; Score 977; DB 16; Length 977;
Matches 977; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60

QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVEPFTPRVLRASSFQISGNPVTLCETQSLERSDVPFRFRDDQTLGLWS 240
DB 181 VKIQVEPFTPRVLRASSFQISGNPVTLCETQSLERSDVPFRFRDDQTLGLWS 240

QY 241 LSPNQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300

QY 301 GTKVTLHCETQDSLTLYRYFHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQDSLTLYRYFHEGVPLRHKSVCRCERGASISFSLTTTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLLIFEGAKVTLHCEAORGSLPILYQFHHDDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLLIFEGAKVTLHCEAORGSLPILYQFHHDDAA 420

QY 421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480
DB 421 LERRSANGAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSIITVPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVQSGSPOLLYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540
DB 481 EALTTEGATVTLHCEVQSGSPOLLYQFVHEDMPLWSSSTPSVGRVSFSLTEGHSNGYY 540

QY 541 CTADNGFGPQRSEVVSFLFVTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSEVVSFLFVTVPSRPILTLRVPRQAQVVGDLLELHCEAPRGSPPILYWF 600

QY 601 YHEDVTLGSSAPSGCEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSAPSGCEASFNLSLTAHSGNYSCEANGLVAQHSDDTISLSVIVPSRPI 660

QY 661 LTRAPRAQAVVGDILLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLITTE 720
DB 661 LTRAPRAQAVVGDILLELHCEALRGSSPILYWFYHEDVTLGKISAPSGGASFNLSLITTE 720

QY 721 HSGIYSCAADNGLEAQRSEMWTLKVAVPVSRPVLTLRAPGTHAAVGDILLELHCEALRGSP 780
DB 721 HSGIYSCAADNGLEAQRSEMWTLKVAVPVSRPVLTLRAPGTHAAVGDILLELHCEALRGSP 780

QY 781 LILYRFHEDVTLGNRSSPSSGGASLNLSTAHSGNYSCEADNGLGAQRSEVTLITGL 840
DB 781 LILYRFHEDVTLGNRSSPSSGGASLNLSTAHSGNYSCEADNGLGAQRSEVTLITGL 840

QY 841 TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRPASDPARSPDSQBPVTH 900
DB 841 TANRSGPFATGVAGGLLSIAGLAAGALLLYCWLRSKAGRPASDPARSPDSQBPVTH 900

QY 901 NVPAMELOQVYTNANPRGENVYSEVRIIOEKKKHAVASDRPHLRNKGSPIIYSEVKVA 960
DB 901 NVPAMELOQVYTNANPRGENVYSEVRIIOEKKKHAVASDRPHLRNKGSPIIYSEVKVA 960

QY 961 STPVSGSLFLASSAPHR 977
DB 961 STPVSGSLFLASSAPHR 977

RESULT 6
US-10-241-220-97
; Sequence 97, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 97
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-97

Query Match
Best Local Similarity 80.7%; Score 788; DB 14; Length 977;
Matches 888; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPQTKWYHR 60

QY 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQSVV 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHPHACLKNGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVEPFTPRVLRASSFQISGNPVTLCETQSLERSDVPFRFRDDQTLGLWS 240
DB 181 VKIQVEPFTPRVLRASSFQISGNPVTLCETQSLERSDVPFRFRDDQTLGLWS 240

QY 241 LSPNQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
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Db 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVISDSRSPWQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLHKSVCERGASISFSLTTSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLHKSVCERGASISFSLTTSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGSPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGSPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Qy 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
Qy 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660
Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE 720
Qy 721 HSGIYCEADNGLEAQRSEMTLVKAVPVSRPILTRAPGTHAAVGDLLHCEALRGSP 780
Db 721 HSGIYCEADNGLEAQRSEMTLVKAVPVSRPILTRAPGTHAAVGDLLHCEALRGSP 780
Qy 781 LILYRFHEDVTLGSRSSPGGASNLSLTAHSGNYSCEADNGLGAORSETVLIYITGL 840
Db 781 LILYRFHEDVTLGSRSSPGGASNLSLTAHSGNYSCEADNGLGAORSETVLIYITGL 840
Qy 841 TANRSGPFATGAVAGLLSITAGLAAGALLLYCWLRSKAGKPKASDPARSP 889
Db 841 TANRSGPFATGAVAGLLSITAGLAAGALLLYCWLRSKAGKPKASDPARSP 889

RESULT 7
US-10-040-862-10460
; Sequence 10460, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040, 862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match 76.4%; Score 746; DB 14; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGOFARTPRFIIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYR 60
Db 1 MLLWVILLVLPVSGOFARTPRFIIIFLOPPWTTVFOGERVTLTCKGFRFYSQKTKWYR 60
Qy 61 YLGEILRETPDNILSVQESGEYRCAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVY 120
Db 61 YLGEILRETPDNILSVQESGEYRCAQGSPLSSPVHLDFSSASLILQAPLSVFEGDSVY 120
Qy 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDFHIFHACLKONGAYRGTGKYKSCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDVLAFLNKRDFHIFHACLKONGAYRGTGKYKSCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLWS 240
Db 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPLRFRFRDDQTLGLWS 240
Qy 241 LSNFOITAMWSKDSGFYWCKAATMPHSVISDSRSPWQVQIPASHPVLTLSPEKALNFE 300
Db 241 LSNFOITAMWSKDSGFYWCKAATMPHSVISDSRSPWQVQIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLHKSVCERGASISFSLTTSNGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLYRFYHEGVPLHKSVCERGASISFSLTTSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGSPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSPHVLNLSPEDLIFEGAKVTLHCEAQRGSPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLITVPSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db 481 EALTFFEGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Qy 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
Db 541 CTADNGFGPQRSEVSLFVTVPVSRPILTLRVPRAQAVVGDLLHCEAPRGSPPILYWF 600
Qy 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660
Db 601 YHEDVTLGSSAPSGGEASFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPVSRI 660
Qy 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE 720
Db 661 LTFRAPRAQAVVGDLLHCEALRGSSPILYFYHEDVTLGKISAPSGGASFNLSLITE 720
Qy 721 HSGIYCEADNGLEAQRSEMTLVKAV 746

Db 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 8

US-10-057-475B-10460

; Sequence 10460, Application US/10057475B

; Publication No. US20040002068A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Mannion, Jane

; APPLICANT: Clapper, Jonathan David

; APPLICANT: Wang, Aijun

; APPLICANT: Ordenez, Nadia

; APPLICANT: Carter, Lauren

; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-014402US

; CURRENT APPLICATION NUMBER: US/10/057,475B

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10460

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-475B-10460

Query Match 76.4%; Score 746; DB 15; Length 759;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLWILLVLAVSQFARTPRPIIFLOPPWTVFQGERVITLCKGFRFYSFQTKWYHR 60

Db 1 MLLWILLVLAVSQFARTPRPIIFLOPPWTVFQGERVITLCKGFRFYSFQTKWYHR 60

Qy 61 YLGKILRTPDNILEVQESGYRCQAGSPLSSVHLDFFSSASLILQAPLSVFEQDSVV 120

Db 61 YLGKILRTPDNILEVQESGYRCQAGSPLSSVHLDFFSSASLILQAPLSVFEQDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKDNVLAFLNKRDTDFH PHACLKDNAGVACTGYKSCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKDNVLAFLNKRDTDFH PHACLKDNAGVACTGYKSCCPVSSNT 180

Qy 181 VKIQVEPTTRPVLRASSQPIISGNPVTITCTQLSLERSDVPLFRFRDDQTLGLGWS 240

Db 181 VKIQVEPTTRPVLRASSQPIISGNPVTITCTQLSLERSDVPLFRFRDDQTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTILHCTQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTEGSGNYCYCTADNG 360

Db 301 GTKVTILHCTQEDSLRTLRYFYHGVPLRHKSVRCERGASISFSLTTEGSGNYCYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHPVNLNLSPPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPSVHPVLTLSA 480

Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLSTVPSVHPVLTLSA 480

Qy 481 EALTPEGATVTLHCEYQRCSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGSGNYCY 540

Db 481 EALTPEGATVTLHCEYQRCSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGSGNYCY 540

Qy 541 CTADNGFGPQSEVSLFVTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRSPPILYWF 600

Db 541 CTADNGFGPQSEVSLFVTVPVSRPILTLRVPRQAQVVGDLLELHCEAPRSPPILYWF 600

Qy 601 YHEDVTLGSSSAPSGGGEASFNLSTLTAHSGNYSCAANGLVAQHSDTISLSIVPVSRPI 660

Db 601 YHEDVTLGSSSAPSGGGEASFNLSTLTAHSGNYSCAANGLVAQHSDTISLSIVPVSRPI 660

Qy 661 LTFRPAQAVVGDLLELHCEALRGSSPILYQFYHEDVTLGKISAPSGGASFNLSLTTE 720

Db 661 LTFRPAQAVVGDLLELHCEALRGSSPILYQFYHEDVTLGKISAPSGGASFNLSLTTE 720

Qy 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

Db 721 HSGIYSCDADNGLEAQRSEWTLKVA 746

RESULT 9

US-10-154-884B-10460

; Sequence 10460, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

Query Match 76.4%; Score 746; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60

QY 61 YLGEILRETPDNILEVQSGEYRCQAQSPSSPVHLDFFSSASLILQAPLSVFEQDSVY 120
DB 61 YLGEILRETPDNILEVQSGEYRCQAQSPSSPVHLDFFSSASLILQAPLSVFEQDSVY 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHI PHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHI PHACLKNDGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVEPTPRVLRASSQPIISGNPVTTCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
DB 181 VKIQVEPTPRVLRASSQPIISGNPVTTCETQLSLERSDVPLRFRFRDDQTLGLGWS 240

QY 241 LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTVVPSHPVNLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVVPSHPVNLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSVTVVPSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSVTVVPSHPVLTLSA 480

QY 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF 600
DB 541 CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF 600

QY 601 YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660

QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYFHEDVTLGKISAPSGGASFNLSLITE 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYFHEDVTLGKISAPSGGASFNLSLITE 720

QY 721 HSGIYSCADNGLAEQRSEMTLKVA 746
DB 721 HSGIYSCADNGLAEQRSEMTLKVA 746

RESULT 10
US-10-403-847-7
; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN
; FILE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 76.4%; Score 746; DB 15; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTKGFRFYSQKTKWYHR 60

QY 61 YLGEILRETPDNILEVQSGEYRCQAQSPSSPVHLDFFSSASLILQAPLSVFEQDSVY 120
DB 61 YLGEILRETPDNILEVQSGEYRCQAQSPSSPVHLDFFSSASLILQAPLSVFEQDSVY 120

QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHI PHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDPHI PHACLKNDGAYRCTGYKESCCPVSSNT 180

QY 181 VKIQVEPTPRVLRASSQPIISGNPVTTCETQLSLERSDVPLRFRFRDDQTLGLGWS 240
DB 181 VKIQVEPTPRVLRASSQPIISGNPVTTCETQLSLERSDVPLRFRFRDDQTLGLGWS 240

QY 241 LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSNFOITAMWSDSGFYWCKAATMPHSVISDSPRSWIQVQIPASHPVLTLSPEKALNFE 300

QY 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360

QY 361 LGAKPSKAVSLSVTVVPSHPVNLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVVPSHPVNLNLSPEDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSVTVVPSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRKAVSLSVTVVPSHPVLTLSA 480

QY 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTFFGATVTLHCEVQRGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF 600
DB 541 CTADNGFGPQRSEVSLFVTVPSRPILTLRVPRAQAVVGDLELHCEAPRSPPILYWF 600

QY 601 YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660
DB 601 YHEDVTLGSSAPSGGEAFNLSLTAHSGNYSCEANGLVAQHSDTISLSVIVPSRPI 660

QY 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYFHEDVTLGKISAPSGGASFNLSLITE 720
DB 661 LTFRAPRAQAVVGDLELHCEALRGSSPILYFYFHEDVTLGKISAPSGGASFNLSLITE 720

QY 721 HSGIYSCADNGLAEQRSEMTLKVA 746
DB 721 HSGIYSCADNGLAEQRSEMTLKVA 746

RESULT 11
US-10-764-324-10460
; Sequence 10460, Application US/10764324

Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US/60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US/60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US/60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US/60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US/60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US/60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US/60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US/60/218,950
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10460
LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 76.4%; Score 746; DB 16; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLWILLVLPVSGQARTPRPIIPLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60
DB 1 MLLWILLVLPVSGQARTPRPIIPLOPPWTTVFQGERVLTCKGFRFYSPQTKWYHR 60

QY 61 YLGKILRETPDNIILEVQESGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFEQDSV 120
DB 61 YLGKILRETPDNIILEVQESGEYRCQAGSPLSPVHLDFFSSASLILQAPLSVFEQDSV 120

QY 121 LRCRAKAEVTLNNTYKQNDVLAFLNKRTPDHI PHACLKQNGAYRCTGKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTYKQNDVLAFLNKRTPDHI PHACLKQNGAYRCTGKESCCPVSSNT 180

QY 181 VKIQVEPTTRVLRASSFPQISGNPNVLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240
DB 181 VKIQVEPTTRVLRASSFPQISGNPNVLTCTETQLSLERSDVPLRFRFRDDQTLGLGWS 240

QY 241 LSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSWTOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSWTOVQIPASHPVLTLSPEKALNFE 300

QY 301 GFKVTLHCETQDSRLTYRFRVHEGVPLRHKSVRCERGASISFSLTTENSGNYICTADNG 360
DB 301 GFKVTLHCETQDSRLTYRFRVHEGVPLRHKSVRCERGASISFSLTTENSGNYICTADNG 360

QY 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILYQPHHEDAA 420
DB 361 LGAKPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCEAQRGSLPILYQPHHEDAA 420

QY 421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFGPQRKAVSLSTVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYICTADNGFGPQRKAVSLSTVTPVSHPVLTLSA 480

QY 481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTTEGATVTLHCEVORGSPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

QY 541 CTADNGFGPQRSEVSLFVTPVRSRPIILTRVPRQAQVAVGDLLELHCEAPRGSPPILYWF 600
DB 541 CTADNGFGPQRSEVSLFVTPVRSRPIILTRVPRQAQVAVGDLLELHCEAPRGSPPILYWF 600

QY 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCAANGLVAQHSOTISLSVIVPVSRI 660
DB 601 YHEDVTILGSSSAPSGGEASFNLSLTAHSGNYSCAANGLVAQHSOTISLSVIVPVSRI 660

QY 661 LTFRAPRAQAVVGDLLELHCEALRGSPILYWFYHEDVTILGKISAPSGGASFNLSLITTE 720
DB 661 LTFRAPRAQAVVGDLLELHCEALRGSPILYWFYHEDVTILGKISAPSGGASFNLSLITTE 720

QY 721 HSGIYSCAENDGLEAQRSEMVTUKVA 746
DB 721 HSGIYSCAENDGLEAQRSEMVTUKVA 746

RESULT 12
US-10-403-847-4
Sequence 4, Application US/10403847
Publication No. US20040030098A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLIC VARIANTS OF A HUMAN
FILE REFERENCE: D0228 NP
CURRENT APPLICATION NUMBER: US/10/403,847
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,671
PRIOR FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: U.S. 60/371,420
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 790
TYPE: PRT
ORGANISM: Homo sapiens
US-10-403-847-4

Query Match 65.9%; Score 644; DB 15; Length 790;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 ASLILQAPLSVFEQDSVLRCAKAEVTLNNTYKQNDVLAFLNKRTPDHI PHACLKQNG 162
DB 134 ASLILQAPLSVFEQDSVLRCAKAEVTLNNTYKQNDVLAFLNKRTPDHI PHACLKQNG 193

QY 163 AYRCTGVKESCCPVSSNTVKIQVEPTTRVLRASSFPQISGNPNVLTCTETQLSLERSDV 222
DB 194 AYRCTGVKESCCPVSSNTVKIQVEPTTRVLRASSFPQISGNPNVLTCTETQLSLERSDV 253

QY 223 PLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSWTOVQI 282
DB 254 PLRFRFRDDQTLGLGWSLSPNFOITAMWSKDSGFYWCXKAATMPHSVSDSPRSWTOVQI 313

QY 283 PASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTYRFRVHEGVPLRHKSVRCERGASIS 342
DB 314 PASHPVLTLSPEKALNFEQTKVTLHCETQDSRLTYRFRVHEGVPLRHKSVRCERGASIS 373

QY 343 FSLTTENSGNYICTADNGLGAQPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCE 402
DB 374 FSLTTENSGNYICTADNGLGAQPSKAVSLSTVTPVSHPVNLSSPEDLIFEPAKVTLHCE 433

QY 403 AQRGSLPILYQPHHEDAAALERRSANSAGGVAISFSLTAHSGNYICTADNGFGPQRKAV 462


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/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10979
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10461
/ LENGTH: 592
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-057-475B-10461

Query Match      57.3%; Score 560; DB 15; Length 592;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFGQERVLTCTCKGFRFYSPOKTKWYHR 60
Db      1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFGQERVLTCTCKGFRFYSPOKTKWYHR 60

Qy      61 YLGKEILRETPDNILEVQESGEYRCAQGSPLSSPVHLDFSSASLILOAPLSVFEQGSV 120
Db      61 YLGKEILRETPDNILEVQESGEYRCAQGSPLSSPVHLDFSSASLILOAPLSVFEQGSV 120

Qy      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKESCCPVSSNT 180
Db      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKESCCPVSSNT 180

Qy      181 VKIQVEPFTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240
Db      181 VKIQVEPFTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240

Qy      241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVIPASHPVLTLSPEKALNFE 300
Db      241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVIPASHPVLTLSPEKALNFE 300

Qy      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360
Db      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360

Qy      361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db      361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy      421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVLTLSA 480
Db      421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVLTLSA 480

Qy      481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db      481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540

Qy      541 CTADNGFGPQRSVSLFVT 560
Db      541 CTADNGFGPQRSVSLFVT 560
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RESULT 15
US-10-154-884B-10461
/ Sequence 10461, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mannion, Jane
```

```
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ TITLE OF INVENTION: Hematological Malignancies
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 11290
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10461
/ LENGTH: 592
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-154-884B-10461

Query Match      57.3%; Score 560; DB 15; Length 592;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFGQERVLTCTCKGFRFYSPOKTKWYHR 60
Db      1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFGQERVLTCTCKGFRFYSPOKTKWYHR 60

Qy      61 YLGKEILRETPDNILEVQESGEYRCAQGSPLSSPVHLDFSSASLILOAPLSVFEQGSV 120
Db      61 YLGKEILRETPDNILEVQESGEYRCAQGSPLSSPVHLDFSSASLILOAPLSVFEQGSV 120

Qy      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKESCCPVSSNT 180
Db      121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKESCCPVSSNT 180

Qy      181 VKIQVEPFTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240
Db      181 VKIQVEPFTPRVLRASSFQPIISGNPVTLTCTQLSLERSDVPFLRFRFRDDOTLGLWS 240

Qy      241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVIPASHPVLTLSPEKALNFE 300
Db      241 LSPNQITAMWSKDSGFYWCKAATMPHSVISDSPRSWIOVIPASHPVLTLSPEKALNFE 300

Qy      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360
Db      301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTTENSGNYICTADNG 360

Qy      361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db      361 LGAKPSKAVSLSVTVPVSHPVNLNLSPPDLIPEGAKVTLHCEAQRGSLPILYQFHEDAA 420

Qy      421 LERRANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPVSHPVLTLSA 480
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Qy      481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
Db      481 EALTPEGATVTLHCEVQSGPQILYQFYHEDMPLWSSSTPSVGRVSFSLTEGHSNYY 540
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Db	541	CTADNGFGPQRSEVVSFLVT	560

Search completed: November 18, 2004, 13:17:17
Job time : 159 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2004, 12:57:59 ; Search time 25 seconds
(without alignments)
2591.707 Million cell updates/sec

Title: US-09-724-254A-41

Perfect score: 977

Sequence: 1 MLLWILLVLAPVSGQFART.....KVASTPVSGSLFLASSAPHR 977

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_AA.*
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6: /cgm2_6/ptodata/1/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	0.9	51	3	US-08-569-147-91
2	9	0.9	107	3	US-08-838-682-16
3	9	0.9	107	3	US-08-895-914-16
4	9	0.9	107	3	US-09-357-710A-16
5	9	0.9	107	4	US-09-357-707-16
6	9	0.9	107	4	US-09-357-708-16
7	9	0.9	109	5	PCT-US92-02044-2
8	9	0.9	121	3	US-08-838-682-11
9	9	0.9	121	3	US-08-895-914-11
10	9	0.9	121	3	US-09-357-710A-11
11	9	0.9	121	4	US-09-357-707-11
12	9	0.9	121	4	US-09-357-708-11
13	8	0.8	36	3	US-09-227-357-550
14	8	0.8	107	2	US-08-888-366-14
15	8	0.8	107	2	US-08-888-366-20
16	8	0.8	107	2	US-08-888-366-26
17	8	0.8	138	4	US-09-252-991A-26931
18	8	0.8	230	3	US-09-485-737B-102
19	8	0.8	233	3	US-09-485-737B-89
20	8	0.8	235	3	US-09-485-737B-93
21	8	0.8	240	3	US-09-485-737B-91
22	8	0.8	261	4	US-09-245-764-7
23	8	0.8	267	3	US-09-485-737B-2
24	8	0.8	469	4	US-09-538-092-948
25	8	0.8	541	3	US-09-485-737B-85
26	8	0.8	711	3	US-09-485-737B-90
27	8	0.8	906	1	US-08-486-270-2

28	8	0.8	906	3	US-08-367-264-2	Sequence 2, Appli
29	8	0.8	906	4	US-09-153-757-2	Sequence 2, Appli
30	8	0.8	906	4	US-09-459-715-2	Sequence 2, Appli
31	8	0.8	906	5	PCT-US91-09422-17	Sequence 17, Appl
32	8	0.8	1056	2	US-08-687-289A-7	Sequence 7, Appli
33	8	0.8	1056	2	US-08-687-289A-8	Sequence 8, Appli
34	8	0.8	1056	4	US-09-435-897-7	Sequence 7, Appli
35	8	0.8	1056	4	US-09-435-897-8	Sequence 8, Appli
36	8	0.8	1194	3	US-08-538-526-1	Sequence 1, Appli
37	8	0.8	1199	1	US-08-041-538-2	Sequence 2, Appli
38	8	0.8	1199	1	US-08-463-642-2	Sequence 2, Appli
39	8	0.8	1199	1	US-08-455-602-2	Sequence 2, Appli
40	8	0.8	1199	2	US-08-465-157-2	Sequence 2, Appli
41	8	0.8	1199	5	PCT-US91-09422-2	Sequence 2, Appli
42	8	0.8	1219	2	US-08-687-289A-6	Sequence 6, Appli
43	8	0.8	1219	4	US-09-435-897-6	Sequence 6, Appli
44	7	0.7	10	3	US-08-581-662-7	Sequence 7, Appli
45	7	0.7	10	4	US-09-664-295-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-569-147-91
; Sequence 91, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-147-91

Query Match 0.9%; Score 9; DB 3; Length 51;
Best Local Similarity 100.0%; Pred No. 0.59; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Cy 37 GERVTLTCK 45
|||||
Db 40 GERVTLTCK 48

RESULT 2

US-08-838-682-16
; Sequence 16, Application US/08895914
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
Db 16 GERVTLTCK 24

RESULT 3
US-08-895-914-16
; Sequence 16, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-914-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
Db 16 GERVTLTCK 24

RESULT 4
US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-16

Query Match 0.9%; Score 9; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GERVTLTCK 45
Db 16 GERVTLTCK 24

RESULT 5

US-09-357-707-16
; Sequence 16, Application US/09357707
; Patent No. 6649163

GENERAL INFORMATION:

APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357,707
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-16

Query Match 0.9%; Score 9; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45

Db 16 GERVLTCK 24

RESULT 6

US-09-357-708-16
; Sequence 16, Application US/09357708
; Patent No. 6770450

GENERAL INFORMATION:

APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-16

Query Match 0.9%; Score 9; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45

Db 16 GERVLTCK 24

RESULT 7

PCT-US92-02044-2
; Sequence 2, Application PC/TUS9202044

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
; APPLICANT: SATO, Vicki L.
; APPLICANT: CHISHOLM, Patricia L.
; APPLICANT: WALLNER, Barbara P.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING
; TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02044
FILING DATE: 19920312
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,975
FILING DATE: 12-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B150CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 715-0600
TELEFAX: (212) 715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-02044-2

Query Match 0.9%; Score 9; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVLTCK 45

Db 16 GERVLTCK 24

RESULT 8

US-08-838-682-11
; Sequence 11, Application US/08938682
; Patent No. 6107090

GENERAL INFORMATION:

APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603-1051
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-682-11

Query Match 0.9%; Score 9; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVTLTK 45
Db 22 GERVTLTK 30
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RESULT 9
US-08-895-914-11
; Sequence 11, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hatgrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-895-914-11

Query Match 0.9%; Score 9; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVTLTK 45
Db 22 GERVTLTK 30
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RESULT 10
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-357-710A-11

Query Match 0.9%; Score 9; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GERVTLTK 45
Db 22 GERVTLTK 30
|||||

RESULT 11
US-09-357-707-11
; Sequence 11, Application US/093577707
; Patent No. 6649163
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357,707
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-11

Query Match      0.9%; Score 9; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37 GERVTLTK 45
Db      22 GERVTLTK 30

RESULT 12
US-09-357-708-11
; Sequence 11, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-11

Query Match      0.9%; Score 9; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37 GERVTLTK 45
Db      22 GERVTLTK 30

RESULT 13
US-09-227-357-550
; Sequence 550, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
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US-08-888-366-14
; Sequence 14, Application US/08888366

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; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 14:
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; TOPOLOGY: linear
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; US-08-888-366-14

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; Patent No. 5972656
; GENERAL INFORMATION:
; APPLICANT: Lopez, Osvaldo
; APPLICANT: Wylie, Dwane E.
; APPLICANT: Wagner, Fred W.
; TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
; CITY: Minneapolis
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; STATE: MN
; COUNTRY: USA
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/888,366
; FILING DATE: 03-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,407
; FILING DATE: 27-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,542
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/493,299
; FILING DATE: 14-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/324,392
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.39USC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
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PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
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PR 08-MAR-1999; 99WO-US005028.
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PR 01-DEC-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US000376.
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PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
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PR 24-AUG-2000; 2000WO-US023328.
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XX DE Novel human secreted or transmembrane protein PRO820.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX Homo sapiens.

XX US2002132252-A1.

PD 19-SEP-2002.

XX 14-NOV-2001; 2001US-00990442.
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XX 17-OCT-1997; 97US-0062250P.
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XX 08-MAR-1999; 99WO-US005028.

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PR 02-JUN-1999; 99WO-US012252.
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 PR 28-JUL-2000; 2000WO-US020710.
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 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021086.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 PA (GETH) GENENTECH INC.
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 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;
 PI Grimaldi JC, Gurney AJ, Kijavini IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;
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 DR WPI: 2003-247083/24.
 DR N-PSDB; ABX80219.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.
 XX
 PS Claim 12; Fig 83; 648pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813
 CC and PRO1065 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or Crohn's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein
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 AC ABUS2589;
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 DT 26-JUN-2003 (first entry)
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 DE Human secreted/transmembrane protein PRO820.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosa; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.
 XX
 OS Homo sapiens.
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 PD 13-FEB-2003.
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 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
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 PR 25-FEB-1998; 98US-0075945P.
 PR 28-MAR-1998; 98US-0078910P.
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 PR 04-JUN-1998; 98US-0088029P.

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GenCore version 5.1.6
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3: pir3:*
4: pir4:*

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and is derived by analysis of the total score distribution.

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41	7	0.7	131	2 S75262	hypothetical prote
42	7	0.7	132	2 I71935	sensory transducti
43	7	0.7	132	2 I71935	MHC class II I-A-a
44	7	0.7	133	2 AB2869	conserved hypotet
45	7	0.7	135	2 B72768	hypothetical prote

ALIGNMENTS

RESULT 1

JC7593
SH2 domain-containing phosphatase anchor protein 1a - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7593
R;Xu, M.; Zhao, R.; Zhao, Z.J.
Biochem. Biophys. Res. Commun. 280, 768-775, 2001
A;Title: Molecular cloning and characterization of SPAP1, an inhibitory receptor.
F;27-135/Domain: extracellular #status predicted <EXT>
F;68-115/Domain: immunoglobulin-like #status predicted <IGL>
F;148-169/Domain: transmembrane region #status predicted <TM>
F;195-255/Domain: intracellular #status predicted <INT>
A;Accession: JC7593
A;Molecule type: mRNA
A;Residues: 1-255 <XUA>
A;Cross-references: UNIPROT:Q9BZ16; GB:AF319438
C;Genetics:
A;Gene: Spapla
A;Map position: 1q21
A;Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3
C;Keywords: glycoprotein
P;27-135/Domain: extracellular #status predicted <EXT>
P;68-115/Domain: immunoglobulin-like #status predicted <IGL>
P;148-169/Domain: transmembrane region #status predicted <TM>
P;195-255/Domain: intracellular #status predicted <INT>

Query Match 2.4%; Score 23; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 618 ASPNLSITAEHSNGYSCAANGL 640
Db 99 ASPNLSITAEHSNGYSCAANGL 121

RESULT 2

D37266
Ig kappa chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: D37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: D37266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
P;19-93/Domain: immunoglobulin homology <IMV>

Query Match 0.9%; Score 9; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;

Query 37 GERVTLTCK 45
 Db 19 GERVTLTCK 27
 |||||

RESULT 3
 I33932
 Ig kappa chain precursor V region (E7) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
 C:Accession: I33932
 R:Baccala, R.; Vo Quang, T.; Gilbert, M.; TERNYNCK, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4824-4828, 1989
 A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line
 A:Reference number: A33932; MUID:89282823; PMID:2499887
 A:Accession: I33932
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-118 <BAC>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:39-113/Domain: immunoglobulin homology <IMM>

Query Match 0.9%; Score 9; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Query 37 GERVTLTCK 45
 Db 39 GERVTLTCK 47
 |||||

RESULT 4
 XNWS21
 Ig kappa chain precursor V region (MOPC 21) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C:Accession: A93736; A90262; B49982; A01917
 R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.
 Nucleic Acids Res. 9, 4485-4494, 1981
 A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxy
 A:Reference number: A93736; MUID:82059477; PMID:6170937
 A:Accession: A93736
 A:Molecule type: mRNA
 A:Residues: 1-136 <HAM>
 A:Cross-references: UNIPROT:P01634
 R:Swasti, J.; Milstein, C.
 Biochem. J. 128, 427-444, 1972
 A:Title: The complete amino acid sequence of a mouse kappa light chain.
 A:Reference number: A90262; MUID:73053310; PMID:4638343
 A:Contents: myeloma protein MOPC 21
 A:Accession: A90262
 A:Molecule type: protein
 A:Residues: 30-136 <SV>
 R:Lin, C.; Kleber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
 J. Biol. Chem. 269, 2805-2813, 1994
 A:Title: Topology of an amiloride-binding protein.
 A:Reference number: A49982; MUID:94132051; PMID:8300613
 A:Accession: B49982
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 30-136 <LIN>
 A:Cross-references: GB:I24803; NID:9452098; PIDN:AAC37684.1; PID:G452099
 A:Experimental source: clone BA7.1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>

F:45-119/Domain: immunoglobulin homology <IMM>
 F:125-136/Region: J segment (JK2)
 F:52-117/Disulfide bonds: #status predicted

Query Match 0.9%; Score 9; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 9; Conservative 0; Indels 0; Gaps 0;

Query 37 GERVTLTCK 45
 Db 45 GERVTLTCK 53
 |||||

RESULT 5
 AC3314
 Hypothetical membrane spanning protein BMEI0497 [imported] - Brucella melitensis (strain
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AC3314
 R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Mazur, M.; Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AC3314
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-167 <KUR>
 A:Cross-references: UNIPROT:Q8VIE7; GB:AE008917; PIDN:AAL51678.1; PID:gl7982410; GSPDB:GB
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0497
 A:Map position: 1

Query Match 0.8%; Score 8; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 15; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

Query 861 GLAAGALL 868
 Db 81 GLAAGALL 88
 |||||

RESULT 6
 E75150
 Hypothetical protein PAB0241 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: E75150
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
 A:Reference number: A75001
 A:Accession: E75150
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-194 <RAW>
 A:Cross-references: UNIPROT:Q9V1R5; GB:AJ248284; GB:AL096836; NID:95457730; PIDN:CAB49284
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB0241

Query Match 0.8%; Score 8; DB 2; Length 194;
 Best Local Similarity 100.0%; Pred. No. 17; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

Query 4 WVILLVLA 11
 Db 27 WVILLVLA 34
 |||||

RESULT 7
 I50609

T-cell surface glycoprotein CD8 beta chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50609; 337237
R:Trigasres, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J.; Immunol. 154, 4485-4494, 1995
A:Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha A lymphocytes.
A:Reference number: I50609; MUID:95238946; PMID:7722305
A:Accession: I50609
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TR>
A:Cross-references: UNIPROT:Q90769; EMBL:Z26484; NID:G403300; PIDN:CAA81258.1; PID:G4033
C:Superfamily: T-cell surface glycoprotein CD8 beta chain; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 0.8%; Score 8; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 LAAGALLL 869
|||
Db 175 LAAGALLL 182

RESULT 8
A34636
Fc-gamma receptor II precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tomimaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K. Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (F3/37-88/Domain: immunoglobulin homology <IMM>
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Accession: A34636
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <TOM>
A:Cross-references: GB:M35272
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 0.8%; Score 8; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 SGEYRQCA 87
|||
Db 81 SGEYRQCA 88

RESULT 9
I55577
Fc gamma (IgG) receptor I-B splice form 1 precursor - human
N:Alternate names: CD64
N:Contains: Fc-gamma (IgG) receptor I-B splice form 2
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55577; I70303
R:Portges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P. J. Clin. Invest. 90, 2102-2109, 1992
A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A:Reference number: I55577; MUID:93055454; PMID:1430234
A:Accession: I55577
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-280 <RES>
A:Cross-references: UNIPROT:Q92637; GB:L03419; NID:G182460; PIDN:AAA35825.1; PID:G292023
A>Note: splice form B1
A:Accession: I70303

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-103-153, 'A', 155-280 <RE2>
A:Cross-references: GB:L03420; NID:G182461; PIDN:AAA35826.1; PID:G292024
A:Experimental source: mononuclear cells
A>Note: splice form B2
C:Comment: This receptor does not bind monomeric IgG with high affinity.
C:Genetics:
A:Gene: GDB:FCGR1B; CD64
A:Cross-references: GDB:135923; OMIM:601502
A:Map position: 1p12-1p12
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 0.8%; Score 8; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 489 TVTLHCEV 496
|||
Db 38 TVTLHCEV 45

RESULT 10
F72759
hypothetical protein APE0067 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: F72759
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: F72759
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-281 <KAW>
A:Cross-references: UNIPROT:Q9YG34; DBJ:AF000058; NID:G5103388; PIDN:BAA78976.1; PID:G51
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0067
C:Superfamily: probable ribose ABC transporter rbsC-2

Query Match 0.8%; Score 8; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 860 AGLAAGAL 867
|||
Db 59 AGLAAGAL 66

RESULT 11
E84310
hypothetical protein Vng1572c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84310
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84310
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <STO>
A:Cross-references: UNIPROT:Q9HPL8; GB:AE004437; NID:G10581055; PIDN:AAG19849.1; GSPDB:G

```
A:Gene: VNG1572C
C:Superfamily: uncharacterized conserved protein MJ1598

Query Match      0.8%; Score 8; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      860 AGLAAGAL 867
DB      178 AGLAAGAL 185
      |||||
      |||||

RESULT 12
E83740
hypothetical protein BH0725 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: E83740
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512562; PMID:11058132
A:Accession: E83740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <STO>
A:Cross-references: UNIPROT:Q9KEX4; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA8044
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0725
C:Superfamily: hypothetical protein yded

Query Match      0.8%; Score 8; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      862 LAAGALLL 869
DB      44 LAAGALLL 51
      |||||
      |||||

RESULT 13
S17952
acyltransferase (EC 2.3.1.-) luxD - Photobacterium leiognathi
C:Species: Photobacterium leiognathi
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S17952
R:Lee, C.Y.; Szittner, R.B.; Meighen, E.A.
Eur. J. Biochem. 201, 161-167, 1991
A:Title: The lux genes of the luminous bacterial symbiont, Photobacterium leiognathi, of
coli.
A:Reference number: S17836; MUID:92007870; PMID:1915359
A:Accession: S17952
A:Molecule type: DNA
A:Residues: 1-315 <LEE>
A:Cross-references: UNIPROT:P21309; EMBL:ME3594; NID:gl50687; PIDN:AAA25617.1; PID:gl506
C:Genetics:
A:Gene: luxD
C:Superfamily: acyltransferase (EC 2.3.1.-) luxD
C:Keywords: acyltransferase

Query Match      0.8%; Score 8; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      387 PEDLIEFG 394
DB      164 PEDLIEFG 171
      |||||
      |||||

RESULT 14
T36841
probable secreted protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36841
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21615
A:Accession: T36841
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-322 <OLI>
A:Cross-references: UNIPROT:O88063; EMBL:AL031541; PIDN:CAA20817.1; SSPDB:GN00070; SCOEDE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDE:SCI35.28

Query Match      0.8%; Score 8; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      611 SAPSGGEA 618
DB      56 SAPSGGEA 63
      |||||
      |||||

RESULT 15
A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N:Alternate names: CD64
C:Species: Homo sapiens (man)
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41357; S03019
R:Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A:Title: Isolation and expression of functional high-affinity Fc receptor complementary I
A:Reference number: A41357; MUID:89100284; PMID:2911749
A:Accession: A41357
A:Molecule type: mRNA
A:Residues: 1-344 <ALLI>
A:Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:gl31333; PIDN:CAA32536.1; P
R:Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FCR)
A:Reference number: S03018; MUID:89098339; PMID:2974947
A:Accession: S03019
A:Molecule type: mRNA
A:Residues: 1-344 <ALL2>
A:Cross-references: EMBL:X14355; NID:gl31333; PIDN:CAA32536.1; PID:gl31334
A:Note: the authors translated the codon ACT for residue 25 as Ala
C:Superfamily: Fc gamma receptor I; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:117-170/Domain: immunoglobulin homology <IMM>

Query Match      0.8%; Score 8; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      489 TVTLHCEV 496
DB      38 TVTLHCEV 45
      |||||
      |||||

Search completed: November 18, 2004, 13:05:53
Job time : 49 secs
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